

DEFINITION	LOCUS	549899	356 bp	DNA	PRT	10-JUL-1992
DEFINITION	alpha-globin gene cluster: {5' region, major regulatory element}					
ACCESSION	human, genomic, 356 nt.					
NID	549899					
KEYWORDS	g233777					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
AUTHORS	1 (bases 1 to 356) Jarnan,A.P., Wood,W.G., Sharpe,J.A., Gourdon,G., Ayub,H. and Higgs,D.R.					
TITLE	Characterization of the major regulatory element upstream of the human alpha-globin gene cluster					
JOURNAL	Mol. Cell. Biol. 11 (9), 4679-4689 (1991)					
MEDLINE	91342671					
REMARK	Genbank staff at the National Library of Medicine created this entry [NCBI glibsq 49899] from the original journal article. This sequence comes from fig 5.					
COMMENT	Region: alpha-globin gene cluster.					
FEATURES	Location/Qualifiers					
source	1..356					
BASE COUNT	89 a 89 c 108 g 70 t					
ORIGIN						
Query Match	98.9%; Score 145.4; DB:40; Length 356;					
Best Local Similarity	99.3%; Pred. No. 7.4e-38;					
Matches 146; Conservative	0; Mismatches 1; Indels 0; Gaps 0;					
Y	1 agataatggtcccaacatgactcagttctctgtgaggtcccaacaggaacttcgagttac					
Db	111 AGATAATGTGGGCCAACCATGACTCAGTCTCTTGAGAGGCCAACAGAGACTGCTGAGTATC					
Y	61 ctgtgtgggtgtgaggtgtgggacaagggaggggtgaatgtagtctgattacaacctt 120					
Db	171 CTGTGGGGGTGTGAGGTGTGGGACAAAGGGAAGGGGTGAATGTGATCGATTTACAACTCT					
Y	121 ggtgtgtcctccccctctctgttatct 147					
Db	231 GGGTCTGCTCCCTCCCTCTCTCTTATCT 257					
RESULT	4					
LOCUS	HS6G4	19226 bp	DNA	PRI	19-MAR-1997	
DEFINITION	Human DNA sequence from cosmid G64 from a contig from the tip of the short arm of chromosome 16, spanning 2mb of 16p13.3.					
ACCESSION	284722					
NID	91817579					
KEYWORDS	16p13.3.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
AUTHORS	1 (bases 1 to 19226) Flint,J. and Higgs,D.R.					
TITLE	Direct Submission					
JOURNAL	Submitted (28-JAN-1997) Sanger Centre, 970124/Hinxton, Cambridgeshire, CB10 1RO, UK. E-mail enquiries: humpb@sanger.ac.uk					
COMMENT	IMPORTANT: This sequence is not the entire insert of clone G64. This clone was sequenced at the Institute of Molecular Medicine. The true left end of clone G64 is at 1 in this sequence. The true right end of clone RA36 is at 456. The true left end of clone PX94 is at 19090. G64 is from a 280kb clone contig extending from the telomere of 16p.					
	Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit, Institute of Molecular Medicine, Oxford.					

GG4 came from the Los Alamos, flow sorted human Chromosome 16 library.

FEATURES
source

Location/Qualifiers
1. .19226
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/chromosome="16"
/map="16p13.3"
/clone="GG4"
601. .894
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1156. .1290
/note="AluX repeat: matches 1. .136 of consensus;
incomplete repeat"
1291. .1601
/note="AluSp repeat: matches 1. .300 of consensus"
1602. .1758
/note="AluSg repeat: matches 132. .288 of consensus;
incomplete repeat"
3487. .3784
/note="AluSg repeat: matches 1. .299 of consensus"
3809. .4104
/note="AluYb repeat: matches 1. .302 of consensus"
4823. .5030
/note="AluSg repeat: matches 2. .208 of consensus;
incomplete repeat"
5053. .5092
/note="20 copies of 2 mer 85 & conserved"
5122. .5280
/note="PAM repeat: matches 164. .5 of consensus"
5759. .5903
/note="L1MC2 repeat: matches 169. .321 of consensus"
6130. .6427
/note="AluSg repeat: matches 297. .1 of consensus"
6428. .6724
/note="AluYb repeat: matches 299. .1 of consensus"
7144. .7255
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7453. .7747
/note="AluSp repeat: matches 1. .303 of consensus"
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/db_xref="PID:g1817580"
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ADNGNSPSPFPHILPCKLRADLRKAYR"
8094. .8307
/note="AluSg repeat: matches 212. .1 of consensus;
incomplete repeat"
8578. .8861
/note="AluY repeat: matches 3. .297 of consensus"
8907. .9210
/note="AluYb repeat: matches 300. .1 of consensus"
9807. .9887
/note="MIR repeat: matches 105. .185 of consensus"
12438. .12731
/note="AluYb repeat: matches 297. .3 of consensus"
12946. .13243
/note="AluSp repeat: matches 299. .2 of consensus"
14000. .14139
/note="AluYb repeat: matches 2. .141 of consensus;
incomplete repeat"
14140. .14453
/note="AluX repeat: matches 1. .302 of consensus"
14454. .14596
/note="L1MB6 repeat: matches 760. .907 of consensus"
16385. .16584
/note="10 copies of 20 mer 91 & conserved"
18800. .19089
/note="AluX repeat: matches 1. .293 of consensus"

Query Match	99.6%;	Score 354.4;	DB 40;	Length 356;
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				Gaps 0;
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Db	1	TCGACCTCTCGAACCTCATATAGGACCAAGATGACCGACAGCACACTTCTGCCAAGCC	60	
OY	61	aagggctggaagcagtcagctctgaggggctctgtgaaaacacttgaggagacagataactgg	120	
Db	61	AAGGCTGAGGCATGACAGCTGTGGGGGCTGTGGAAACCTTGAGGGAGCGAGTAATCTGG	120	
OY	121	gccaacatgactcagctgctctcggagggcaacagagactctcgatcactcctgtgggggt	180	
Db	121	GCCAACCATGATCATGCTTCTTCTGGAGGCCAACAGAGACTGTGATCATCTCTGTGGGGGT	180	
OY	181	ggaagttggagaaagggaaaggggtgaattgtctgtgtgttaacaacctgtgtctcct	240	
Db	181	GAGGTGGAGAAAGGAAAGGGGATGATGTACTCTGATTAACAACCTCTGTGTCTCCT	240	

Oy	241	ccccctccttattatcgaggaaggacacgcccagaagtgttcacagccgttcag	300
Db	241	ccccctccttattatcgaggaaggacacgcccagaagtgttcacagccgttcag	300
Oy	301	gggcacaagctgcaccacagactaatcacyttcttcaccttgagctgaagaattc	356
Db	301	gggcacaagctgcaccacagactaatcacyttcttcaccttgagctgaagaattc	356
RESULT	4		
HSGG4		19226 bp	DNA
LOCUS			PRI 19-MAR-1997
DEFINITION		Human DNA sequence from cosmid G64 from a contig from the tip of the short arm of chromosome 16, spanning 2kb of 16p13.3.	
ACCESSION		Z84722	
NID		g1817579	
KEYWORDS		16p13.3.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1. (bases 1 to 19226)	
AUTHORS		Flint,J. and Higgs,D.R.	
TITLE		Direct Submission	
JOURNAL		Submitted (28-JAN-1997) Sanger Centre, 970124/Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquiries: humpub@sanger.ac.uk IMPORTANT: This sequence is not the entire insert of clone G64. This clone was sequenced at the Institute of Molecular Medicine. The true left end of clone G64 is at 1 in this sequence. The true right end of clone RA36 is at 456. The true left end of clone PY44 is at 19090. G64 is from a 280kb clone contig extending from the telomere of 16p.	
COMMENT		Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit, Institute of Molecular Medicine, Oxford. G64 came from the Los Alamos, flow sorted human Chromosome 16 library.	
FEATURES		Location/Qualifiers	
source		1. 19226 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="16" /map="16p13.3" /map="G64" /clone="G64" .894 /note="AluB repeat: matches 301. .5 of consensus" 1156. 1290 /note="AluX repeat: matches 1. .136 of consensus; incomplete repeat" 1291. 1601 /note="AluSp repeat: matches 1. .300 of consensus" 1602. 1758 /note="AluSg repeat: matches 132. .288 of consensus; incomplete repeat" 3487. 3784 /note="AluSg repeat: matches 1. .299 of consensus" 3809. 4104 /note="AluI repeat: matches 1. .302 of consensus" 4823. 5030 /note="AluSg repeat: matches 2. .208 of consensus; incomplete repeat" 5053. 5092 /note="20 copies of 2 mer 85 & conserved" 5122. 5280 /note="FAM repeat: matches 164. .5 of consensus" 5759. 5903 /note="LIMC2 repeat: matches 169. .321 of consensus" 6130. 6427 /note="AluSg repeat: matches 297. .1 of consensus" 6428. 6724 /note="AluI repeat: matches 299. .1 of consensus" 7144. 7265	